

Favouritism and secret crosstalk in diatom–bacteria relations

Stock Willem¹, Frederik De Boever¹, Anne Willems², Sven Mangelinckx³, Marleen De Troch⁴, Wim Vyverman¹, and Koen Sabbe¹

¹ Laboratory of Protistology and Aquatic Ecology, Biology Department, Ghent University, Krijgslaan 281 – S8, B–9000 Ghent, Belgium
E-mail: Willem.Stock@UGent.be

² Laboratory of Microbiology (LM–UGent), Department of Biochemistry and Microbiology, Ghent University, K.L. Ledeganckstraat 35, B–9000 Ghent, Belgium

³ SynBioC, Department of Sustainable Organic Chemistry and Technology, Faculty of Bioscience Engineering, Ghent University, Coupure Links 653, B–9000 Ghent, Belgium

⁴ Marine Biology, Biology Department, Ghent University, Krijgslaan 281 – S8, B–9000 Ghent, Belgium

Diatoms are the most successful group of eukaryotic microalgae in today's oceans: they are responsible for one fifth of the global oxygen production and play a vital role in the carbon cycle. The co-occurrence of diatoms and bacteria over evolutionary time-scales has resulted in strong interactions. It has even been argued that these interactions are one of the reasons behind the success of the diatoms.

While many aspects of these interactions still need to be investigated, the degree of specificity between the diatom host and its associated bacteria is of particular interest. It has been shown that only a small number of bacterial genera are consistently observed in diatom–bacteria consortia, suggesting that these organisms have coevolved.

To determine the processes driving these specific interactions, we are characterizing the bacterial communities associated with >80 closely related diatom strains. By comparing the composition of the bacterial communities with the evolutionary tree of their hosts, we will assess to what degree host identity and phylogeny determine bacterial community composition, and compare it with the influence of environmental and geographic parameters.

In parallel, we are studying the mechanisms underlying diatom–bacteria interactions by setting up co-cultures. Through one-on-one co-culture experiments, we are comparing the effect that bacteria have on their native host with the effect they have on a foreign host. Using metabolomic approaches we are assessing the involvement of signalling mechanisms (i.c. bacterial quorum sensing molecules) in the host–bacterium interaction.